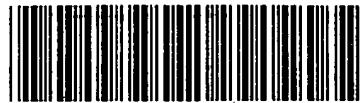*KW*

PCT09

ENTERED

RAW SEQUENCE LISTING   DATE: 02/13/2002
PATENT APPLICATION: US/09/743,825   TIME: 07:58:02

          Input Set : A:\seqlist.txt
          Output Set: N:\CRF3\02132002\I743825.raw

```
 4 <110> APPLICANT: Chuaqui, Rodrigo F.
 5         Cole, Kristina A.
 6         Liotta, Lance A.
 9 <120> TITLE OF INVENTION: PB39, A Gene Dysregulated in Prostate
10         Cancer and Uses Thereof
13 <130> FILE REFERENCE: 66043 /US
15 <140> CURRENT APPLICATION NUMBER: 09/743,825
16 <141> CURRENT FILING DATE: 1999-07-23
18 <150> PRIOR APPLICATION NUMBER: US 60/094,137
19 <151> PRIOR FILING DATE: 1998-07-24
21 <150> PRIOR APPLICATION NUMBER: PCT/US99/16831
22 <151> PRIOR FILING DATE: 1999-07-23
24 <160> NUMBER OF SEQ ID NOS: 17
26 <170> SOFTWARE: FastSEQ for Windows Version 3.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 2326
30 <212> TYPE: DNA
31 <213> ORGANISM: Homo sapiens
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (77)...(1753)
37 <400> SEQUENCE: 1
38  ccggggctgg aggggggcaa gcgggttccg aggtgcaaag cctggtgccc cgagccctgc     60
39  ggagctcggg gccagc atg gcc ccc acg ctg caa cag gcg tac cgg agg cgc    112
40                    Met Ala Pro Thr Leu Gln Gln Ala Tyr Arg Arg Arg
41                     1               5                   10
43  tgg tgg atg gcc tgc acg gct gtg ctg gag aac ctc ttc ttc tct gct    160
44  Trp Trp Met Ala Cys Thr Ala Val Leu Glu Asn Leu Phe Phe Ser Ala
45           15                  20                  25
47  gta ctc ctg ggc tgg ggc tcc ctg ttg atc att ctg aag aac gag ggc    208
48  Val Leu Leu Gly Trp Gly Ser Leu Leu Ile Ile Leu Lys Asn Glu Gly
49        30                  35                  40
51  ttc tat tcc agc acg tgc cca gct gag agc agc acc aac acc acc cag    256
52  Phe Tyr Ser Ser Thr Cys Pro Ala Glu Ser Ser Thr Asn Thr Thr Gln
53     45                  50                  55                  60
55  gat gag cag cgc agg tgg cca ggc tgt gac cag cag gac gag atg ctc    304
56  Asp Glu Gln Arg Arg Trp Pro Gly Cys Asp Gln Gln Asp Glu Met Leu
57                  65                  70                  75
59  aac ctg ggc ttc acc att ggt tcc ttc gtg ctc agc gcc acc acc ctg    352
60  Asn Leu Gly Phe Thr Ile Gly Ser Phe Val Leu Ser Ala Thr Thr Leu
61                  80                  85                  90
63  cca ctg ggg atc ctc atg gac cgc ttt ggc ccc cga ccc gtg cgg ctg    400
64  Pro Leu Gly Ile Leu Met Asp Arg Phe Gly Pro Arg Pro Val Arg Leu
```

```
65            95                    100                   105
67  gtt ggc agt gcc tgc ttc act gcg tcc tgc acc ctc atg gcc ctg gcc      448
68  Val Gly Ser Ala Cys Phe Thr Ala Ser Cys Thr Leu Met Ala Leu Ala
69       110                    115                  120
71  tcc cgg gac gtg gaa gct ctg tct ccg ttg ata ttc ctg gcg ctg tcc      496
72  Ser Arg Asp Val Glu Ala Leu Ser Pro Leu Ile Phe Leu Ala Leu Ser
73  125                    130                    135                140
75  ctg aat ggc ttt ggt ggc atc tgc cta acg ttc act tca ctc acg ctg      544
76  Leu Asn Gly Phe Gly Gly Ile Cys Leu Thr Phe Thr Ser Leu Thr Leu
77                     145                    150                155
79  ccc aac atg ttt ggg aac ctg cgc tcc acg tta atg gcc ctc atg att      592
80  Pro Asn Met Phe Gly Asn Leu Arg Ser Thr Leu Met Ala Leu Met Ile
81                160                    165                    170
83  ggc tct tac gcc tct tct gcc att acg ttc cca gga atc aag ctg atc      640
84  Gly Ser Tyr Ala Ser Ser Ala Ile Thr Phe Pro Gly Ile Lys Leu Ile
85           175                    180                    185
87  tac gat gcc ggt gtg gcc ttc gtg gtc atc atg ttc acc tgg tct ggc      688
88  Tyr Asp Ala Gly Val Ala Phe Val Val Ile Met Phe Thr Trp Ser Gly
89       190                    195                    200
91  ctg gcc tgc ctt atc ttt ctg aac tgc acc ctc aac tgg ccc atc gaa      736
92  Leu Ala Cys Leu Ile Phe Leu Asn Cys Thr Leu Asn Trp Pro Ile Glu
93  205                    210                    215                220
95  gcc ttt cct gcc cct gag gaa gtc aat tac acg aag aag atc aag ctg      784
96  Ala Phe Pro Ala Pro Glu Glu Val Asn Tyr Thr Lys Lys Ile Lys Leu
97                 225                    230                    235
99  agt ggg ctg gcc ctg gac cac aag gtg aca ggt gac ctc ttc tac acc      832
100 Ser Gly Leu Ala Leu Asp His Lys Val Thr Gly Asp Leu Phe Tyr Thr
101                240                    245                    250
103 cat gtg acc acc atg ggc cag agg ctc agc cag aag gcc ccc agc ctg      880
104 His Val Thr Thr Met Gly Gln Arg Leu Ser Gln Lys Ala Pro Ser Leu
105           255                    260                    265
107 gag gac ggt tcg gat gcc ttc atg tca ccc cag gat gtt cgg ggc acc      928
108 Glu Asp Gly Ser Asp Ala Phe Met Ser Pro Gln Asp Val Arg Gly Thr
109      270                    275                    280
111 tca gaa aac ctt cct gag agg tct gtc ccc tta cgc aag agc ctc tgc      976
112 Ser Glu Asn Leu Pro Glu Arg Ser Val Pro Leu Arg Lys Ser Leu Cys
113 285                    290                    295                300
115 tcc ccc act ttc ctg tgg agc ctc ctc acc atg ggc atg acc cag ctg     1024
116 Ser Pro Thr Phe Leu Trp Ser Leu Leu Thr Met Gly Met Thr Gln Leu
117                305                    310                    315
119 cgg atc atc ttc tac atg gct gct gtg aac aag atg ctg gag tac ctt     1072
120 Arg Ile Ile Phe Tyr Met Ala Ala Val Asn Lys Met Leu Glu Tyr Leu
121                320                    325                    330
123 gtg act ggt ggc cag gag cat gag aca aat gaa cag caa caa aag gtg     1120
124 Val Thr Gly Gly Gln Glu His Glu Thr Asn Glu Gln Gln Gln Lys Val
125           335                    340                    345
127 gca gag aca gtt ggg ttc tac tcc tcc gtc ttc ggg gcc atg cag ctg     1168
128 Ala Glu Thr Val Gly Phe Tyr Ser Ser Val Phe Gly Ala Met Gln Leu
129      350                    355                    360
```

```
131  ttg tgc ctt ctc acc tgc ccc ctc att ggc tac atc atg gac tgg cgg    1216
132  Leu Cys Leu Leu Thr Cys Pro Leu Ile Gly Tyr Ile Met Asp Trp Arg
133  365                 370                 375                 380
135  atc aag gac tgc gtg gac gcc cca act cag ggc act gtc ctc gga gat    1264
136  Ile Lys Asp Cys Val Asp Ala Pro Thr Gln Gly Thr Val Leu Gly Asp
137                  385                 390                 395
139  gcc agg gac ggg gtt gct acc aaa tcc atc aga cca cgc tac tgc aag    1312
140  Ala Arg Asp Gly Val Ala Thr Lys Ser Ile Arg Pro Arg Tyr Cys Lys
141                  400                 405                 410
143  atc caa aag ctc acc aat gcc atc agt gcc ttc acc ctg acc aac ctg    1360
144  Ile Gln Lys Leu Thr Asn Ala Ile Ser Ala Phe Thr Leu Thr Asn Leu
145              415                 420                 425
147  ctg ctt gtg ggt ttt ggc atc acc tgt ctc atc aac aac tta cac ctc    1408
148  Leu Leu Val Gly Phe Gly Ile Thr Cys Leu Ile Asn Asn Leu His Leu
149          430                 435                 440
151  cag ttt gtg acc ttt gtc ctg cac acc att gtt cga ggt ttc ttc cac    1456
152  Gln Phe Val Thr Phe Val Leu His Thr Ile Val Arg Gly Phe Phe His
153  445                 450                 455                 460
155  tca gcc tgt ggg agt ctc tat gct gca gtg ttc cca tcc aac cac ttt    1504
156  Ser Ala Cys Gly Ser Leu Tyr Ala Ala Val Phe Pro Ser Asn His Phe
157                  465                 470                 475
159  ggg acg ctg aca ggc ctg cag tcc ctc atc agt gct gtg ttc gcc ttg    1552
160  Gly Thr Leu Thr Gly Leu Gln Ser Leu Ile Ser Ala Val Phe Ala Leu
161                  480                 485                 490
163  ctt cag cag cca ctt ttc atg gcg atg gtg gga ccc ctg aaa gga gag    1600
164  Leu Gln Gln Pro Leu Phe Met Ala Met Val Gly Pro Leu Lys Gly Glu
165              495                 500                 505
167  ccc ttc tgg gtg aat ctg ggc ctc ctg cta ttc tca ctc ctg gga ttc    1648
168  Pro Phe Trp Val Asn Leu Gly Leu Leu Leu Phe Ser Leu Leu Gly Phe
169          510                 515                 520
171  ctg ttg cct tcc tac ctc ttc tat tac cgt gcc cgg ctc cag cag gag    1696
172  Leu Leu Pro Ser Tyr Leu Phe Tyr Tyr Arg Ala Arg Leu Gln Gln Glu
173  525                 530                 535                 540
175  tac gcc gcc aat ggg atg ggc cca ctg aag gtg ctt agc ggc tct gag    1744
176  Tyr Ala Ala Asn Gly Met Gly Pro Leu Lys Val Leu Ser Gly Ser Glu
177                  545                 550                 555
179  gtg acc gca tagacttctc agaccaaggg acctggatga caggcaatca            1793
180  Val Thr Ala
183  aggcctgagc aaccaaaagg agtgccccat atggctttc  tacctgtaac atgcacatag  1853
184  agccatggcc gtagatttat aaataccaag agaagttcta tttttgtaaa gactgcaaaa  1913
185  aggaggaaaa aaaaccttca aaaacgcccc ctaagtcaac gctccattga ctgaagacag  1973
186  tccctatcct agaggggttg agctttcttc ctccttgggt tggaggagac cagggtgcct  2033
187  cttatctcct tctagcggtc tgcctcctgg tacctcttgg ggggatcggc aaacaggcta  2093
188  cccctgaggt cccatgtgcc atgagtgtgc acaacatgca atgtgtctgt gtatgtgtga  2153
189  atgtgagaaa aacacagccc tcctttcaga aggaaagggg cctgaggtgc cagctgtgtc  2213
190  ctgggttagg ggttgggggt cggccccttc caggccagg  aaggcaggtt ccctctctgg  2273
191  tgctgctgct tgcaagtctt agaggaaata aaaagggaag tgagaaaaaa aaa          2326
193  <210> SEQ ID NO: 2
194  <211> LENGTH: 559
```

```
195 <212> TYPE: PRT
196 <213> ORGANISM: Homo sapiens
198 <400> SEQUENCE: 2
199 Met Ala Pro Thr Leu Gln Gln Ala Tyr Arg Arg Arg Trp Trp Met Ala
200  1               5                   10                  15
201 Cys Thr Ala Val Leu Glu Asn Leu Phe Phe Ser Ala Val Leu Leu Gly
202              20                  25                  30
203 Trp Gly Ser Leu Leu Ile Ile Leu Lys Asn Glu Gly Phe Tyr Ser Ser
204          35                  40                  45
205 Thr Cys Pro Ala Glu Ser Ser Thr Asn Thr Thr Gln Asp Glu Gln Arg
206      50                  55                  60
207 Arg Trp Pro Gly Cys Asp Gln Gln Asp Glu Met Leu Asn Leu Gly Phe
208 65                  70                  75                  80
209 Thr Ile Gly Ser Phe Val Leu Ser Ala Thr Thr Leu Pro Leu Gly Ile
210              85                  90                  95
211 Leu Met Asp Arg Phe Gly Pro Arg Pro Val Arg Leu Val Gly Ser Ala
212             100                 105                 110
213 Cys Phe Thr Ala Ser Cys Thr Leu Met Ala Leu Ala Ser Arg Asp Val
214             115                 120                 125
215 Glu Ala Leu Ser Pro Leu Ile Phe Leu Ala Leu Ser Leu Asn Gly Phe
216         130                 135                 140
217 Gly Gly Ile Cys Leu Thr Phe Thr Ser Leu Thr Leu Pro Asn Met Phe
218 145                 150                 155                 160
219 Gly Asn Leu Arg Ser Thr Leu Met Ala Leu Met Ile Gly Ser Tyr Ala
220             165                 170                 175
221 Ser Ser Ala Ile Thr Phe Pro Gly Ile Lys Leu Ile Tyr Asp Ala Gly
222             180                 185                 190
223 Val Ala Phe Val Val Ile Met Phe Thr Trp Ser Gly Leu Ala Cys Leu
224             195                 200                 205
225 Ile Phe Leu Asn Cys Thr Leu Asn Trp Pro Ile Glu Ala Phe Pro Ala
226         210                 215                 220
227 Pro Glu Glu Val Asn Tyr Thr Lys Lys Ile Lys Leu Ser Gly Leu Ala
228 225                 230                 235                 240
229 Leu Asp His Lys Val Thr Gly Asp Leu Phe Tyr Thr His Val Thr Thr
230             245                 250                 255
231 Met Gly Gln Arg Leu Ser Gln Lys Ala Pro Ser Leu Glu Asp Gly Ser
232             260                 265                 270
233 Asp Ala Phe Met Ser Pro Gln Asp Val Arg Gly Thr Ser Glu Asn Leu
234             275                 280                 285
235 Pro Glu Arg Ser Val Pro Leu Arg Lys Ser Leu Cys Ser Pro Thr Phe
236         290                 295                 300
237 Leu Trp Ser Leu Leu Thr Met Gly Met Thr Gln Leu Arg Ile Ile Phe
238 305                 310                 315                 320
239 Tyr Met Ala Ala Val Asn Lys Met Leu Glu Tyr Leu Val Thr Gly Gly
240             325                 330                 335
241 Gln Glu His Glu Thr Asn Glu Gln Gln Gln Lys Val Ala Glu Thr Val
242             340                 345                 350
243 Gly Phe Tyr Ser Ser Val Phe Gly Ala Met Gln Leu Leu Cys Leu Leu
244             355                 360                 365
```

```
245  Thr Cys Pro Leu Ile Gly Tyr Ile Met Asp Trp Arg Ile Lys Asp Cys
246      370             375             380
247  Val Asp Ala Pro Thr Gln Gly Thr Val Leu Gly Asp Ala Arg Asp Gly
248  385             390             395             400
249  Val Ala Thr Lys Ser Ile Arg Pro Arg Tyr Cys Lys Ile Gln Lys Leu
250              405             410             415
251  Thr Asn Ala Ile Ser Ala Phe Thr Leu Thr Asn Leu Leu Leu Val Gly
252              420             425             430
253  Phe Gly Ile Thr Cys Leu Ile Asn Asn Leu His Leu Gln Phe Val Thr
254      435             440             445
255  Phe Val Leu His Thr Ile Val Arg Gly Phe Phe His Ser Ala Cys Gly
256      450             455             460
257  Ser Leu Tyr Ala Ala Val Phe Pro Ser Asn His Phe Gly Thr Leu Thr
258  465             470             475             480
259  Gly Leu Gln Ser Leu Ile Ser Ala Val Phe Ala Leu Leu Gln Gln Pro
260              485             490             495
261  Leu Phe Met Ala Met Val Gly Pro Leu Lys Gly Glu Pro Phe Trp Val
262              500             505             510
263  Asn Leu Gly Leu Leu Leu Phe Ser Leu Leu Gly Phe Leu Leu Pro Ser
264      515             520             525
265  Tyr Leu Phe Tyr Tyr Arg Ala Arg Leu Gln Gln Glu Tyr Ala Ala Asn
266      530             535             540
267  Gly Met Gly Pro Leu Lys Val Leu Ser Gly Ser Glu Val Thr Ala
268  545             550             555
270  <210> SEQ ID NO: 3
271  <211> LENGTH: 3442
272  <212> TYPE: DNA
273  <213> ORGANISM: Homo sapiens
275  <220> FEATURE:
276  <221> NAME/KEY: CDS
277  <222> LOCATION: (1760)...(3439)
279  <400> SEQUENCE: 3
280  ccggggctgg aggggggcaa gcgggttccg aggtgcaaag cctggtgccc cgagccctgc       60
281  ggagctcggg gccagcatgg cccccacgct gcaacaggcg taccggaggc gctggtggat      120
282  ggcctgcacg gctgtgctgg agaacctctt cttctctgct gtactcctgg gctggggctc      180
283  cctgttgatc attctgaaga acgagggctt ctattccagc acgtgcccag ctgagagcag      240
284  caccaacacc acccaggatg agcagcgcag gtggccaggc tgtgaccagc aggacgagat      300
285  gctcaacctg ggcttcacca ttggttcctt cgtgctcagc gccaccaccc tgccactggg      360
286  gatcctcatg gaccgctttg gcccccgacc cgtgcggctg gttggcagtg cctgcttcac      420
287  tgcgtcctgc accctcatgg ccctggcctc ccgggacgtg gaagctctgt ctccgttgat      480
288  attcctggcg ctgtccctga atggctttgg tggcatctgc ctaacgttca cttcactcac      540
289  gctgcccaac atgtttggga acctgcgctc cacgttaatg gccctcatga ttggctctta      600
290  cgcctcttct gccattacgt tcccaggaat caagctgatc tacgatgccg gtgtggcctt      660
291  cgtggtcatc atgttcacct ggtctggcct ggcctgcctt atctttctga actgcaccct      720
292  caactggccc atcgaagcct ttcctgcccc tgaggaagtc aattacacga agaagatcaa      780
293  gctgagtggg ctggccctgg accacaaggt gacaggtgac ctcttctaca cccatgtgac      840
294  caccatgggc cagaggctca gccagaaggc ccccagcctg gaggacggtt cggatgcctt      900
295  catgtcaccc caggatgttc ggggcacctc agaaaacctt cctgagaggt ctgtcccctt      960
296  acgcaagagc ctctgctccc ccactttcct gtggagcctc ctcaccatgg gcatgaccca     1020
```

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/743,825

DATE: 02/13/2002
TIME: 07:58:03

Input Set : **A:\seqlist.txt**
Output Set: **N:\CRF3\02132002\I743825.raw**